SEQUENCE LISTING

<110>   Duke University
        York, John D

<120>   NOVEL TARGETS FOR LITHIUM THERAPY AND TOXICITY TREATMENT

<130>   180/158/2

<150>   US 60/401480
<151>   2002-08-06

<160>   24

<170>   PatentIn version 3.2

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gaaaagccat agcaggagtt attaaccagc catattacaa ctatgaggca ggaccagatg   600

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ataagattat tcagctgatt gaaggcaaag cctctgctta tgtatttgca agtcctggtt   840

gtaagaagtg ggatacttgt gctccagaag ttatttttaca tgctgtggga ggcaagttaa   900

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<220>
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            20                  25                  30


Gly Asp Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr
         35                  40                  45


Lys Ala Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg
    50                  55                  60

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu
65                  70                  75                  80


Glu Val Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu
                85                  90                  95
```

2

Lys Gln Pro Cys Pro Ser Gln Tyr Ser Ala Ile Lys Glu Glu Asp Leu
            100   105   110

Val Val Trp Val Asp Pro Leu Asp Gly Thr Lys Glu Tyr Thr Glu Gly
            115   120   125

Leu Leu Asp Asn Val Thr Val Leu Ile Gly Ile Ala Tyr Glu Gly Lys
            130   135   140

Ala Ile Ala Gly Val Ile Asn Gln Pro Tyr Tyr Asn Tyr Glu Ala Gly
145   150   155   160

Pro Asp Ala Val Leu Gly Arg Thr Ile Trp Gly Val Leu Gly Leu Gly
            165   170   175

Ala Phe Gly Phe Gln Leu Lys Glu Val Pro Ala Gly Lys His Ile Ile
            180   185   190

Thr Thr Thr Arg Ser His Ser Asn Lys Leu Val Thr Asp Cys Val Ala
            195   200   205

Ala Met Asn Pro Asp Ala Val Leu Arg Val Gly Gly Ala Gly Asn Lys
            210   215   220

Ile Ile Gln Leu Ile Glu Gly Lys Ala Ser Ala Tyr Val Phe Ala Ser
225   230   235   240

Pro Gly Cys Lys Lys Trp Asp Thr Cys Ala Pro Glu Val Ile Leu His
            245   250   255

Ala Val Gly Gly Lys Leu Thr Asp Ile His Gly Asn Val Leu Gln Tyr
            260   265   270

His Lys Asp Val Lys His Met Asn Ser Ala Gly Val Leu Ala Thr Leu
            275   280   285

Arg Asn Tyr Asp Tyr Tyr Ala Ser Arg Val Pro Glu Ser Ile Lys Asn
            290   295   300

Ala Leu Val Pro
305

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<220>
<221>   MISC_FEATURE

3

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<220>
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<222>   (8)..(8)
<223>   X is isoleucine or an amino acid that can be conservatively
        substituted in place thereof.

<220>
<221>   MISC_FEATURE
<222>   (10)..(10)
<223>   X is glycine or an amino acid that can be conservatively
        substituted in place thereof.

<220>
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<222>   (11)..(11)
<223>   X is threonine or an amino acid that can be conservatively
        substituted in place thereof.

<220>
<221>   MISC_FEATURE
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<223>   X is any number of integers of any amino acid.

<220>
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<223>   X is tryptophan or an amino acid that can be conservatively
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        substituted in place thereof.

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<222>   (15)..(25)
<223>   X is any amino acid.

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Asp Xaa Glu Glu Xaa Asp Pro Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly
            20                  25


<210>   4
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<212>   PRT
<213>   Artificial

<220>
<223>   Li-sensitive sequence uniting motif for Impase1.
```

4

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<223>  X is any amino acid.

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<223>  X is any amino acid.

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1                   5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa
        35                  40                  45


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    50                  55                  60


Xaa Xaa Xaa Xaa Xaa Glu Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65                  70                  75                  80


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Pro Ile Asp Gly Thr Xaa
                85                  90                  95


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            100                 105                 110


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        115                 120                 125


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    130                 135                 140
```

5

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145   150   155   160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                165   170   175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                180   185   190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                195   200   205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Asp Xaa Xaa Xaa Xaa
        210   215   220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225   230   235   240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                245   250   255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                260   265   270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        275   280   285

Xaa Xaa
    290

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<223>   X is any amino acid.

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<223>   X is any amino acid.

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<223>  X is any amino acid.

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<222>  (330)..(399)
<223>  X is any amino acid.

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1                   5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        35                  40                  45


Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    50                  55                  60


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Glu
65                  70                  75                  80


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            85                  90                  95


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        100                 105                 110


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        115                 120                 125


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    130                 135                 140


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Pro Ile Asp Ser Thr Xaa Xaa
145                 150                 155                 160


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            165                 170                 175


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            180                 185                 190


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        195                 200                 205
```

7

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    210                 215                 220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225                 230                 235                 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                245                 250                 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                260                 265                 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            275                 280                 285

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            290                 295                 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Asp Xaa Xaa Xaa Xaa
305                 310                 315                 320

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                325                 330                 335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            340                 345                 350

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            355                 360                 365

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
385                 390                 395
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8

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            20                  25                  30


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        35                  40                  45


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    50                  55                  60


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa
65                  70                  75                  80


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            85                  90                  95


Xaa Glu Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            100                 105                 110


Xaa Xaa Xaa Xaa Xaa Xaa Asp Pro Leu Asp Gly Ser Xaa Xaa Xaa Xaa
            115                 120                 125


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    130                 135                 140


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145                 150                 155                 160


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            165                 170                 175
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9

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        180   185   190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        195   200   205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    210   215   220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225   230   235   240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            245   250   255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        260   265   270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        275   280   285

Xaa Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    290   295   300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
305   310   315   320

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            325   330   335

Xaa Xaa

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<213>   artificial

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<210>   8
<211>   55
<212>   DNA
<213>   artificial

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<223>   5' DNA PCR primer.

<400>   8
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<211>  49
<212>  DNA
<213>  artificial

<220>
<223>  5' DNA PCR primer

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agatctttca attgaagctt gtcgaccagc atgtcgggga tcaagaagc                49


<210>  10
<211>  48
<212>  DNA
<213>  artificial

<220>
<223>  5' DNA PCR primer.

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agatctaagc ttccgcggtc gacctggagc caaaggctta gttcttct                 48


<210>  11
<211>  31
<212>  DNA
<213>  artificial

<220>
<223>  5' DNA PCR primer

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<210>  12
<211>  43
<212>  DNA
<213>  artificial

<220>
<223>  5' DNA PCR primer.

<400>  12
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<210>  13
<211>  31
<212>  DNA
<213>  artificial

<220>
<223>  5' DNA PCR primer.

<400>  13
ggatccaagc acactgtaca ccaatggcta c                                   31


<210>  14
<211>  42
<212>  DNA
<213>  artificial

<220>
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11

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<210> 15
<211> 31
<212> DNA
<213> artificial

<220>
<223> 5' DNA PCR primer.

<400> 15
atcgatcata tggagccctt gcgtaaacca c   31

<210> 16
<211> 22
<212> DNA
<213> artificial

<220>
<223> 5' DNA PCR primer

<400> 16
tcatatttga cagcggaacg tg   22

<210> 17
<211> 981
<212> DNA
<213> artificial

<220>
<223> Fragment of BPntase genomic DNA located between exons 5 and 6
      with 5' and 3' engineered restriction sites.

<400> 17
gtagcacctc acatactctc ccagctccag agctaggccc ctcctgggga atcactgttg   60

tacacttcct ttcctgaggg actgtgctga catgtctgac tgggctagag aaatgctcca   120

ccacccctgg tcccatagca tcccctcacc tgaggttgtc acaggtaaga aaaccagaag   180

gcatcgaatt aaatccagag gtgtaaaagt caggaggagt tgtgtgagag ctcacacctg   240

taatctcagc acactggggc agagggactg ctttgagttt gaggccatct tgagtgctat   300

acatggcaag ttctgggtca gcttgggtta gagcaagacc ttttctaggc aaagcaagac   360

attagtcaga agaacccagt ctcagagctg gacttcgggt tttatttgtt tgtttgtttg   420

tttttatttt ttgagacagg gtttctctgt gtagccctgg ttgtcctggc actcactttg   480

tagaccagac tggcctcgaa ctcagaaatc tgcctgcctc tgcctcccga gtgctgggat   540

taaaggtgtg cgccaccact gcctggctta gacttcaagt tttaaaagcc tagagttgta   600

gttttgaaat aaagatctgc attgagaact tgtgaggctg aggcaggaag actgtgaggt   660

cagcctggcc ttcacagtga gtttcaggtc agcctgagat agaggagcag tgtgaggcca   720

gaaggacccc acaaagaaag acctccacag cgctgcttct aacgggtcca gcttcgagag   780

gctttctcac agctgccaga gagaatgttg ttggcccctg gaggagatag agtgatagtg   840

12

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actctgtgtg tgtgtgtgta aatatatact gtatatactg tgagggtgca tgtgtgcaac    900

atgcatatgt actgtgaaaa tgtgtgagag gcagtgtgtt cgtatgtgtg tctgtgagta    960

taacccatgc gtatgtaatc t                                             981
```

```
<210>  18
<211>  35
<212>  DNA
<213>  artificial

<220>
<223>  5' DNA PCR primer

<400>  18
ggcgcgccgt agcacctcac atactctccc agctc                               35
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```
<210>  19
<211>  34
<212>  DNA
<213>  artificial

<220>
<223>  3' DNA PCR primer

<400>  19
ggcgcgccag attacatacg catgggttat actc                                34
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<210>  20
<211>  4858
<212>  DNA
<213>  artificial

<220>
<223>  Fragment of the genomic BPntase sequence with engineered 5' and
       3' flanking restriction sites.

<400>  20
tggcgagctt gcttattctg ctttcagagt atggggttgt ataaagcacg tggcgccaca     60

ctggggtttc ccgactctta gcccatttaa agcaggttgg aatctagagc gttatgaaag    120

agtttctcaa ttagagaaga gaatattcca aataatttaa aagcaccttt gcaaacttga    180

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13

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